

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 8, 2004, 05:41:17 ; Search time 78 Seconds
(without alignments)
1060.098 Million cell updates/sec

Title: US-09-659-379-6_COPY_27_175

Perfect score: 819
Sequence: 1 EBSOKLPPSSRITCPQGSVA.....OKMRDFNCENLPTICKRV 149

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09659379/rnat 30072004.175948.21071/app.query.fasta_1.327
-DB=Issued Patents NA -OPM=fastap -SUFFIX=tni -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blotsum62 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US09659379.@cgn 1.1.69 @matat 30072004.175948.21071 -NCPU=6 -ICPU=3
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPO2=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA: *
1: /cgn2_6/prodata/2/ina/5A.COMB.seq: *
2: /cgn2_6/prodata/2/ina/5B.COMB.seq: *
3: /cgn2_6/prodata/2/ina/6A.COMB.seq: *
4: /cgn2_6/prodata/2/ina/6B.COMB.seq: *
5: /cgn2_6/prodata/2/ina/6C.COMB.seq: *
6: /cgn2_6/prodata/2/ina/6D.COMB.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	819	100.0	558	1	US-08-909-725-4
2	819	100.0	586	3	US-09-146-969-3
3	819	100.0	747	2	US-08-401-530A-1
4	819	100.0	747	2	US-08-709-662-1
5	511	62.4	474	1	US-07-778-156-8
6	511	62.4	474	2	US-08-422-166-8
7	511	62.4	793	1	US-07-778-156-1
8	511	62.4	793	2	US-08-422-166-1
9	491	60.0	797	2	US-08-464-637-1
10	491	60.0	797	2	US-08-822-261-5
11	491	60.0	797	4	US-09-226-852-5
12	485	59.2	522	1	US-07-778-156-4

13	485	59.2	522	2	US-08-422-166-4	Sequence 4, Appli
14	485	59.2	762	2	US-08-822-261-2	Sequence 2, Appli
15	485	59.2	762	4	US-09-226-852-2	Sequence 2, Appli
16	485	59.2	798	1	US-07-778-156-12	Sequence 12, Appli
17	485	59.2	798	2	US-08-822-261-6	Sequence 6, Appli
18	485	59.2	798	2	US-08-422-166-12	Sequence 12, Appli
19	485	59.2	798	4	US-09-146-969-2	Sequence 2, Appli
20	485	59.2	798	3	US-09-146-969-2	Sequence 2, Appli
21	361	40.1	602	3	US-09-385-982-257	Sequence 257, App
22	333.5	40.7	777	3	US-09-146-969-1	Sequence 1, Appli
23	276.5	33.8	590	2	US-08-454-557C-32	Sequence 32, Appli
24	276.5	33.8	590	2	US-08-340-426D-32	Sequence 32, Appli
25	276.5	33.8	590	2	US-08-450-673C-32	Sequence 32, Appli
26	276.5	33.8	590	5	PCT-US95-17111A-32	Sequence 32, Appli
27	249.5	30.5	610	3	US-09-385-982-229	Sequence 229, Appli
28	198.5	24.2	378	2	US-08-454-557C-16	Sequence 16, Appli
29	198.5	24.2	378	2	US-08-340-426D-16	Sequence 16, Appli
30	198.5	24.2	378	2	US-08-450-673C-16	Sequence 16, Appli
31	198.5	24.2	378	5	PCT-US95-17111A-16	Sequence 16, Appli
32	186.5	22.8	614	2	US-08-729-103-2	Sequence 2, Appli
33	186.5	22.8	1114	2	US-08-468-413-1	Sequence 1, Appli
34	186.5	22.8	1114	3	US-09-162-508-1	Sequence 1, Appli
35	186.5	22.8	1114	5	PCT-US95-07169-1	Sequence 1, Appli
36	173	21.1	544	4	US-09-058-740-1	Sequence 2, Appli
37	166.5	20.3	508	4	US-09-621-976-952	Sequence 952, App
38	161	19.7	5169	4	US-09-194-612A-2	Sequence 2, Appli
39	157	19.2	4588	3	US-08-840-062-1	Sequence 1, Appli
40	156	19.0	4471	3	US-09-146-969-4	Sequence 4, Appli
41	156	19.0	4771	3	US-08-840-062-3	Sequence 3, Appli
42	156	19.0	5633	4	US-09-023-655-1490	Sequence 1490, Ap
43	151	18.4	622	3	US-09-385-982-224	Sequence 224, App
44	149.5	18.3	690	2	US-08-612-840A-7	Sequence 7, Appli
45	149.5	18.3	5191	1	US-08-340-428B-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-909-725-4
; Sequence 4, Application US/08909725
; Patent No. 5804421
GENERAL INFORMATION:
APPLICANT: Vinitk, Aaron
APPLICANT: Pittenger, Gary
APPLICANT: Rateloff-Phail, Ronit
APPLICANT: Barlow, Scott
TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF
TITLE OF INVENTION: INGNP IN BACTERIAL AND EUKARYOTIC CELLS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Wilcoff, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/909,725
FILING DATE: 12-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/741,096
FILING DATE: 30-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32,145
REFERENCE/DOCKET NUMBER: 0570.05173
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 97430 BMB UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 558 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-909-725-4

Alignment Scores:

Pred. No.:	1,94e-90	Length:	558
Score:	819.00	Matches:	149
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1	Indels:	0
		Gaps:	0

US-09-659-379-6_COPY_27_175 (1-149) x US-08-909-725-4 (1-558)

QY 1 GluGluSerGlnLysLeuProSerSerArgIleThrCysProGlnGlySerValAla 20
DB 12 GAAGATCTCAAAAGAACTGCTCTTCTACGTAATACCTGCTCAAGGCTCTGTACCC 71
QY 21 TyrGlySerTyrCysTyrSerLeuIleLeuIleProGlnThrTyrSerAsnAlaGluLeu 40
DB 72 TATGGGCTCTATGCTATTCATGATTTTGATACACAGACTGCTCTTAATGACAGACTA 131
QY 41 SerCysGlnMetHisPheSerGlyHisLeuAlaPheLeuSerThrGlyGluIleThr 60
DB 132 TCCTCCAGATGCAATTTCTCAGACACCTGGCATTTCTCTAGACTGGTGAATAC 191
QY 61 PheValSerSerLeuValLysAsnSerLeuThrAlaTyrGlnTyrIleTyrIleGlyLeu 80
DB 192 TTCGGTCTCTCCCTTGTGAAGACAGTTGACGGCTTACATTCATGATGAGTAC 251
QY 81 HisAppProSerHisGlyThrLeuProAsnGlySerGlyTyrLysTyrSerSerAsn 100
DB 252 CATGATCCCTCAATGATGACACTACCAACGAGATGAGAGAGAGAGAGATTCAT 311
QY 101 ValLeuThrPheTyrAsnTyrGlnLysProSerIleAlaAlaAspArgGlyTyrCys 120
DB 312 GGTGCTACCTTCTATTAACCTGGAGAGAACCCCTCTATGCTGCTCAACCTGTTATGT 371
QY 121 AlaValLeuSerGlnLysSerGlyPheGlnLysTyrPArgAspPheAsnCysGluAsnGlu 140
DB 372 GCAGTTTGTCTCAGAAATCAGCTTTTTCAGAGTGGAGAGATTTTAAATGTGAAAAATGAG 431
QY 141 LeuProTyrIleCysLysPheLysVal 149
DB 432 CTTCCTATATCTGCAAAATTCAGAGTC 458

RESULT 2

US-09-146-969-3
Sequence 3, Application US/09146969
Patent No. 6228585
GENERAL INFORMATION:
APPLICANT: Dieckraefe, Brian K.
TITLE OF INVENTION: Gene Markers for Chronic Mucosal Injury
FILE REFERENCE: 04255.75314
CURRENT APPLICATION NUMBER: US/09/146,969
CURRENT FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 586
TYPE: DNA
ORGANISM: Homo sapiens
US-09-146-969-3

Alignment Scores:

Pred. No.:	2.08e-90	Length:	586
Score:	819.00 <td>Matches:</td> <td>149</td>	Matches:	149
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3	Indels:	0
		Gaps:	0

US-09-659-379-6_COPY_27_175 (1-149) x US-09-146-969-3 (1-586)

QY 1 GluGluSerGlnLysLeuProSerSerArgIleThrCysProGlnGlySerValAla 20
DB 72 GAAGATCTCAAAAGAACTGCTCTTCTACGTAATACCTGCTCAAGGCTCTGTACCC 131
QY 21 TyrGlySerTyrCysTyrSerLeuIleLeuIleProGlnThrTyrSerAsnAlaGluLeu 40
DB 132 TATGGGCTCTATGCTATTCATGATTTTGATACACAGACTGCTCTTAATGACAGACTA 191
QY 41 SerCysGlnMetHisPheSerGlyHisLeuAlaPheLeuSerThrGlyGluIleThr 60
DB 192 TCCTCCAGATGCAATTTCTCAGACACCTGGCATTTCTTCAATGATGAGATTCAC 251
QY 61 PheValSerSerLeuValLysAsnSerLeuThrAlaTyrGlnTyrIleTyrIleGlyLeu 80
DB 252 TCCTGCTCTCCCTTGTGAAGACAGTTGACGGCTTACATTCATGATGAGTAC 311
QY 81 HisAppProSerHisGlyThrLeuProAsnGlySerGlyTyrLysTyrSerSerAsn 100
DB 312 CATGATCCCTCAATGATGACACTACCAACGAGATGAGAGAGATTCAT 371
QY 101 ValLeuThrPheTyrAsnTyrGlnLysProSerIleAlaAlaAspArgGlyTyrCys 120
DB 372 GGTGCTACCTTCTATTAACCTGGAGAGAACCCCTCTATGCTGCTCAACCTGTTATGT 431
QY 121 AlaValLeuSerGlnLysSerGlyPheGlnLysTyrPArgAspPheAsnCysGluAsnGlu 140
DB 432 GCAGTTTGTCTCAGAAATCAGCTTTTTCAGAGTGGAGAGATTTTAAATGTGAAAAATGAG 491
QY 141 LeuProTyrIleCysLysPheLysVal 149
DB 492 CTTCCTATATCTGCAAAATTCAGAGTC 518

RESULT 3

US-08-401-530A-1
Sequence 1, Application US/08401530A
Patent No. 5834590
GENERAL INFORMATION:
APPLICANT: Vainik, Aaron I.
APPLICANT: Pittenger, Gary L.
APPLICANT: Rafaeloff, Ronit
APPLICANT: Rosenberg, Lawrence
APPLICANT: Duguid, William P.
TITLE OF INVENTION: IN GAP PROTEIN INVOLVED IN PANCREATIC
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Banner & Allegretti
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: US
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,530A
FILING DATE: 22-FEB-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 00570.48743
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 747 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Cricetus
FEATURE:
NAME/KEY: CDS
LOCATION: 20..541
US-08-401-530A-1

Alignment Scores:
Pred. No.: 3e-90 Length: 747
Score: 819.00 Matches: 149
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-659-379-6_COPY 27_175 (1-149) x US-08-401-530A-1 (1-747)

QY 1 GluGluSerGlnLysLeuProSerSerArgIleThrCysProGlnGlySerValAla 20
Db 95 GAAGAATCTCAAAAGAAATCGCTTCTTCACTATTAACCTCTCTCAAGGCTCTGTACC 154
QY 21 TyrGlySerTyrCysTyrSerLeuIleLeuIleProGlnThrTPSerAsnIleGluLeu 40
Db 155 TATGGGTCTTATTCCTTCACTGATTTGATACCAAGACCTGGTCTAATGACAGAACTA 214
QY 41 SerCysGlnMetHisPheSerGlyHisLeuAlaPheLeuLeuSerThrGlyGluIleThr 50
Db 215 TCCGCGCAGATGATCTTCTCGAGACCTGGCATTTCTTCTCACTGCTGGAATTAAC 274
QY 61 PheValSerSerLeuValLysAsnSerLeuThrAlaTyrGlnTyrIleTyrIleGlyLeu 80
Db 275 TTGCTGCTCTCCCTTGTGAAGAACAGTTTGACGGCTTACAGATACATCTGATTGACCTC 334
QY 81 HisAspProSerHisGlyThrLeuProAsnGlySerGlyTyrIleTyrTPSerSerAsn 100
Db 335 CATGATCCCTCAATGATGACCACTAACCAGGAAGTGAATGAGAGCAATTCAT 394
QY 101 ValLeuThrPheTyrAsnTyrGluArgAsnProSerIleAlaAlaAspArgGlyTyrCys 120
Db 395 GTGCTGACCTTCTTAACTGGAGAGAACCCCTTAATTCCTGTCGCTGATTATTTGT 454
QY 121 AlValLeuSerGlnLysSerGlyPheGlnLysTyrArgAspPheAsnCysGluAsnGlu 140
Db 455 GCAGTTTGTCTCAGAAATCAGGTTTTCAGAGTGAAGAGATTTAATTGTAATGAG 514
QY 141 LeuProTyrIleCysIlePheVal 149
Db 515 CTTCCTATATCTGCAAAATTCAGAGTC 541

RESULT 4

US-08-709-662-1
Sequence 1, Application US/08709662
Patent No. 5840531
GENERAL INFORMATION:
APPLICANT: Vinik, Aaron I.
APPLICANT: Pittenger, Gary L.
APPLICANT: Rafealoff, Ronit
APPLICANT: Rosenberg, Lawrence
APPLICANT: Duguid, William P.
TITLE OF INVENTION: INGP PROTEIN INVOLVED IN PANCREATIC

TITLE OF INVENTION: ISLET NEOGENESIS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: US
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,662
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 00570.59178
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 747 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Cricetus
FEATURE:
NAME/KEY: CDS
LOCATION: 20..541
US-08-709-662-1

Alignment Scores:
Pred. No.: 3e-90 Length: 747
Score: 819.00 Matches: 149
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-659-379-6_COPY 27_175 (1-149) x US-08-709-662-1 (1-747)

QY 1 GluGluSerGlnLysLeuProSerSerArgIleThrCysProGlnGlySerValAla 20
Db 95 GAAGAATCTCAAAAGAAATCGCTTCTTCACTATTAACCTCTCTCAAGGCTCTGTACC 154
QY 21 TyrGlySerTyrCysTyrSerLeuIleLeuIleProGlnThrTPSerAsnIleGluLeu 40
Db 155 TATGGGTCTTATTCCTTCACTGATTTGATACCAAGACCTGGTCTAATGACAGAACTA 214
QY 41 SerCysGlnMetHisPheSerGlyHisLeuAlaPheLeuLeuSerThrGlyGluIleThr 60
Db 215 TCCGCGCAGATGATCTTCTCGAGACCTGGCATTTCTTCTCACTGCTGGAATTAAC 274
QY 61 PheValSerSerLeuValLysAsnSerLeuThrAlaTyrGlnTyrIleTyrIleGlyLeu 80
Db 275 TTGCTGCTCTCCCTTGTGAAGAACAGTTTGACGGCTTACAGATACATCTGATTGACCTC 334
QY 81 HisAspProSerHisGlyThrLeuProAsnGlySerGlyTyrIleTyrTPSerSerAsn 100
Db 335 CATGATCCCTCAATGATGACCACTAACCAGGAAGTGAATGAGAGCAATTCAT 394
QY 101 ValLeuThrPheTyrAsnTyrGluArgAsnProSerIleAlaAlaAspArgGlyTyrCys 120

Db 395 GTGCTGACCTTCTTAAGTGGAGAGAACCCCTCTATGCTGCTGACCGGTATTGT 454
QY 121 AlaValIeuSerGlnYsSerGlyPheGlnYsTrpArgAspPheAsnCyGluAsnGlu 140
Db 455 GCAGTTTGTCTCGAAGATCAGGTTTTCAGAGTGGAGAGATTTTAATTGGAATAAG 514
QY 141 LeuProTyrIleCyGlyPheVal 149
Db 515 CTTCCTATATCTGCAAAATTCAGGTC 541

RESULT 5
US-07-778-156-8
; Sequence 8, Application US/07778156
; Patent No. 5436169
; GENERAL INFORMATION:
; APPLICANT: IOVANNA, JUAN-LUCIO
; APPLICANT: KEIM, VOLKER
; APPLICANT: DAGORN, JEAN-CHARLES
; TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
; TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
; TITLE OF INVENTION: PANCREATITIS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/778,156
; FILING DATE: 19911219

CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5436169man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 354-012-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 474 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: rat
; TISSUE TYPE: pancreas
; US-07-778-156-8

Alignment Scores:
Pred. No.: 4,166-53 Length: 474
Score: 511.00 Matches: 87
Percent Similarity: 77.70% Conservative: 28
Best Local Similarity: 58.78% Mismatches: 32
Query Match: 62.39% Indels: 1
Gaps: 0

US-09-659-379-6_COPY_27_175 (1-149) X US-07-778-156-8 (1-474)
QY 1 GlnGluSerGlnYsLeuProSerSerArgIleThrCySProGlnGlySerValAla 20
Db 1 GAAGACTCTCGAAGAAATACCTCTGACGATTAAGTCCCAAGGCTCCAGGCA 60

QY 21 TyrIleSerTyrCySlySerIleuIleuIleProGlnThrTrpSerAsnAlaGluLeu 40
Db 61 TATGCTCTCACTCTATAGCCCTGTTTCAGATACACAGACTGTTGATGACGAACTG 120
QY 41 SerCyGlnMetHisPheSerGlyHisLeuAlaPheLeuSerThrGluIleThr 60
Db 121 GCCTGCCAAGAGAGACCTGGAAGACACCTTATCTGCTCATGTACGCAAGCTTCA 180
QY PheValSerSerLeuValIysAsnSerIleuThrAlaTyrGlnIleTyrIleGlyLeu 80
Db 181 TTCTTGATCCATGATGATCAAGACACCTGGAACAGCTACCAATATACCTGATGGACTC 240
QY 81 HisAppProSerHisGlyThrLeuProAsnGlySerGlyTyrIlePylsTrpSerSerAsn 100
Db 241 CATGACCCCTCTGCTGGAGAACCCATGAGTGGATGAGTGGAGTGAACATATAC 300
QY 101 ValIeuThrPheTyrAsnTrpGluArgAsnProSerIleAlaIAspArgGlyTyrCyS 120
Db 301 ATAATGAATTATGTCACTGAGAGAGAACCATCTATGCTTACGCGGATTTCTGT 360
QY 121 AlaValIeuSerGlnYsSerGlyPheGlnYsTrpArgAspPheAsnCyGluAsnGlu 140
Db 361 GCAGCTTGTCAAGATCTTCTGATTTCTTAAGATGAGAGATACCAATGTAAGTTGA 420
QY 141 -LeuProTyrIleCySlyPhe 147
Db 421 GTTGCCCTACGCTGCAAAATTT 442

RESULT 6
US-08-422-166-8
; Sequence 8, Application US/08422166
; Patent No. 5959086
; GENERAL INFORMATION:
; APPLICANT: IOVANNA, JUAN-LUCIO
; APPLICANT: KEIM, VOLKER
; APPLICANT: DAGORN, JEAN-CHARLES
; TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
; TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
; TITLE OF INVENTION: PANCREATITIS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,166
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/778,156
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5959086man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 354-012-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 474 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown

TOPOLOGY: unknown
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: rat
 TISSUE TYPE: pancreas
 US-08-422-166-8

Alignment Scores:
 Pred. No.: 4.16e-53 Length: 474
 Score: 511.00 Matches: 87
 Percent Similarity: 77.70% Conservative: 28
 Best Local Similarity: 58.78% Mismatches: 32
 Query Match: 62.39% Indels: 1
 Gaps: 0

US-09-659-379-6_COPY_27_175 (1-149) x US-08-422-166-8 (1-474)

QY 1 GIUGLISERGLINLYSLYSEUPROSERSEARGLIETHRCYSPROGLINGLYSERVALA 20
 Db 1 GAGAGCTCTCCGAGAGAAATATCCCTCTGCAGCATTAAGTGGCCCAAGGCTCCAGGCA 50
 QY 21 TYRGLYSERTYCYSTYRSERLEULEULEIPROGLINTHTPSEASNAIAGULEU 40
 Db 61 TATGCTCTTACTGCTATGCCCTGTTTCAGATACACAGACCTGGTTTGATGACAGACTG 120
 QY 41 SERCYGLIMETHISPHESERGLYHISLEUALAPHELEUSERTHRGYLULEIETHR 50
 Db 121 GCCGCCAGAGAGAGACCTGAGAGACACCTGTATCTGTGCTCAATGCTGAAAGCTTCA 180
 QY 61 PHEVALSERSEULEVALYSAENSERLEUTHRALATYRGLINTHTPILLEGLYLEU 30
 Db 181 TTCTTGCACTCCAGAGAAATATCCCTCTGCAGCATTAAGTGGCCCAAGGCTCCAGGCA 240
 QY 81 HISAPPROSEHISGLYTHIRLEUPROASNGLYSERGLYTPYLSSTPSEASERASN 100
 Db 241 CATGACCCCACTCTGTTGAGAGACCAATGAGAGTGGAGTGGAGTGAACATGAC 300
 QY 101 VALLEUTHRPHETRYAANTPGIUAARGANPROSERILEA1A1AASPARGGLYTYR 120
 Db 301 ATATGAAATATGATCAACTGGAGAGAGACCAATCTACTCTTACGCCGAGATTCTGT 360
 QY 121 ALVALLEUSERGLINLYSSERGLYPHEGLINLYSTRPARGASPHEANCYSGIUAINGLU 140
 Db 361 GGCAGCTTGCAAGATCTTCTGATTTCTAAGATGAGAGATACCAATGTAAGTTGAA 420
 QY 141 -LEUPROTYRILECYSLYSPHE 147
 Db 421 GTTGCCCTACGTCTGCAAAATT 442

RESULT 7
 US-07-778-156-1

/ Sequence 1, Application US/07778156
 / Patent No. 5436169
 / GENERAL INFORMATION:
 / APPLICANT: IOVANA, JUAN-LUCIO
 / APPLICANT: KEIM, VOLKER
 / APPLICANT: DAGORN, JEAN-CHARLES
 / TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
 / TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
 / NUMBER OF SEQUENCES: 12
 / CORRESPONDENCE ADDRESS:
 / ADDRESSES: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 / ADDRESS: P.C.
 / STREET: 1755 Jefferson Davis Highway, Fourth Floor
 / CITY: Arlington
 / STATE: Virginia
 / COUNTRY: U.S.A.
 / ZIP: 22202
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/778,156
 FILING DATE: 19911219
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, No. 5436169man F.
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 354-012-0 PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703)521-4500
 TELEFAX: (703)486-2347
 TELEX: 248855 OPAT UR
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 793 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: cDNA to mRNA
 ORIGINAL SOURCE:
 ORGANISM: rat
 TISSUE TYPE: pancreas
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 62..613
 US-07-778-156-1

Alignment Scores:
 Pred. No.: 9.02e-53 Length: 793
 Score: 511.00 Matches: 87
 Percent Similarity: 77.70% Conservative: 28
 Best Local Similarity: 58.78% Mismatches: 32
 Query Match: 62.39% Indels: 1
 Gaps: 0

US-09-659-379-6_COPY_27_175 (1-149) x US-07-778-156-1 (1-793)

QY 1 GIUGLISERGLINLYSLYSEUPROSERSEARGLIETHRCYSPROGLINGLYSERVALA 20
 Db 140 GAGAGCTCTCCGAGAGAAATATCCCTCTGCAGCATTAAGTGGCCCAAGGCTCCAGGCA 199
 QY 21 TYRGLYSERTYCYSTYRSERLEULEULEIPROGLINTHTPSEASNAIAGULEU 40
 Db 200 TATGCTCTTACTGCTATGCCCTGTTTCAGATACACAGACCTGGTTTGATGACAGACTG 259
 QY 41 SERCYGLIMETHISPHESERGLYHISLEUALAPHELEUSERTHRGYLULEIETHR 60
 Db 260 GCCGCCAGAGAGAGACCTGAGAGACACCTGTATCTGTGCTCAATGCTGAAAGCTTCA 319
 QY 61 PHEVALSERSEULEVALYSAENSERLEUTHRALATYRGLINTHTPILLEGLYLEU 80
 Db 320 TTCTTGCACTCCAGAGAAATATCCCTCTGCAGCATTAAGTGGCCCAAGGCTCCAGGCA 379
 QY 81 HISAPPROSEHISGLYTHIRLEUPROASNGLYSERGLYTPYLSSTPSEASERASN 100
 Db 380 CATGACCCCACTCTGTTGAGAGACCAATGAGAGTGGAGTGGAGTGAAGTGAACATGAC 439
 QY 101 VALLEUTHRPHETRYAANTPGIUAARGANPROSERILEA1A1AASPARGGLYTYR 120
 Db 440 ATATGAAATATGATCAACTGGAGAGAGAACCAATCTACTGCTTACCGCGGATTCTGT 499
 QY 121 ALVALLEUSERGLINLYSSERGLYPHEGLINLYSTRPARGASPHEANCYSGIUAINGLU 140
 Db 500 GGCAGCTTGCAAGATCTTCTGATTTCTAAGATGAGAGATACCAATGTAAGTTGAA 559
 QY 141 -LEUPROTYRILECYSLYSPHE 147
 Db 560 GTTGCCCTACGTCTGCAAAATT 581

RESULT 8
 US-08-422-166-1
 / Sequence 1, Application US/08422166

Patent No. 5959086
GENERAL INFORMATION:
APPLICANT: IOYANNA, JUAN-LUCIO
APPLICANT: KEIM, VOLKER
APPLICANT: DAGORN, JEAN-CHARLES
TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
TITLE OF INVENTION: PANCREATITIS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,166
FILING DATE: 14-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/778,156
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5959086man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 354-012-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-4500
TELEFAX: (703) 486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: cDNA to mRNA
ORGANISM: rat
TISSUE TYPE: pancreas
FEATURE:
NAME/KEY: CDS
LOCATION: 62..613
US-08-422-166-1
Alignment Scores:
Pred. No.: 9.02e-53 Length: 793
Score: 511.00 Matches: 87
Percent Similarity: 77.70% Conservative: 28
Best Local Similarity: 58.78% Mismatches: 32
Query Match: 62.39% Indels: 1
DB: 2 Gaps: 0
US-09-659-379-6_COPY 27_175 (1-149) x US-08-422-166-1 (1-793)
CY 1 GluGluSerGlnIysLysLeuProSerSerArgIleThrCysProGlnGlySerValAla 20
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DB 140 GAAAGACTCTCGAAGAAATACCTCTGACGCGATTAGTGGCCCAAGGCTCCAGGCA 199
21 TyrGlySerIYrCYrTYrSerLeuIleLeuIleProGlnInhrTrpSerAnaIaGluLeu 40
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 200 TATGGCTCTACTGCTGTAGCCCTGTTTCAGTATCACACAGACCTGTGATGACAGAACTG 259
41 SerCysGlnMetHisPheSerGlyHisLeuAlaPheLeuLeuSerThrGlyGluIleThr 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 260 GCGTCCGCAAGAGACCTCGAAGGACACCTTGTATCTGTGCTCATATGAGTGAAGCTTCA 319

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QY 61 PheValIserSerLeuValIysAsnSerIleuThraAlaTyrGlnTYrIleTPpilEGlyLeu 80
Db 320 TTTCTTGGCATTCATGCTGCTACAGAACCACTACGAAACAGCTACCAATATACCTGGATTGGACTC 379
QY 81 HisAspProSerHisGlyTYrIleuProAsnGlySerGlyTYrIlySTPSeSerSerAsn 100
Db 380 CATGACCCCACTCTGGTGAGAACCCCAATGAGGTGATGGATGGAGCTGGAGTGAATCAATGAC 439
QY 101 ValIleuThPheTYrAsnTrpGluArgAsnProSerIleAlaIAspArgGlyTYrCys 120
Db 440 ATATCAATATATGTCAACTGGAGAGAACCCATCTACTGCTTAGACCGGAGATTCTGT 499
QY 121 AlaValIleuSerGlnIlySerGlyPheGlnIlySTPArgAspPheAsnCysGluAsnGlu 140
Db 500 GGCAGCTTGTCAGAACTTCTGGATTCTTAAGATGAGAGATCACCATGTGAAGTTGAA 559
QY 141 -IleuProTYrIleCysIysPhe 147
Db 560 GTTGCCCTACGCTCTGCAAAATT 581

RESULT 9
US-08-464-637-1
Sequence 1, Application US/08464637
Patent No. 5834214
GENERAL INFORMATION:
APPLICANT: Iovanna, Juan-Lucio
APPLICANT: Dagorn, Jean-Charles
APPLICANT: Keim, Volker
APPLICANT: Sales, Jacques
TITLE OF INVENTION: Detection of Pancreatitis-Associated
TITLE OF INVENTION: Protein for diagnosis of Cystic Fibrosis or Pancreatic
TITLE OF INVENTION: Disease (as amended).
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSER: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-3487
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,637
FILING DATE: 30-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 2121-107P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8050
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 797 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 43..567
OTHER INFORMATION: /product= "human
OTHER INFORMATION: pancreatitis-associated protein"

```

100

STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/226,852
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/822,261
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0251 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 797 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 262368
US-09-226-852-5

Alignment Scores:
Pred. No.: 2,45e-50 Length: 797
Score: 491.00 Matches: 82
Percent Similarity: 77.55% Conservative: 32
Best Local Similarity: 55.78% Mismatches: 33
Query Match: 59.95% Indels: 0
Gaps: 0
DB:

US-09-659-379-6_COPY_27_175 (1-149) x US-09-226-852-5 (1-797)

QY 1 GluGluSerGlnIlySLeuProSerArgIleThrCysProGlnIlySerValAla 20
DB 121 GAAGAACCCCAAGAGGAACTGCTCGAAGATCCGCTGCCAAGGCTCCAGGCC 180
QY 21 TyrGlySerTyrCysTyrSerLeuIleLeuIleProGlnIlyThrPheSerAlaGluLeu 40
DB 181 TATGGCTCCCACTGATGCTGTTTGTTCACCAAAATCTGGACAGATGAGATCTG 240
QY 41 SerCysGlnMetHisPheSerGlyHisLeuAlaPheLeuSerThrGlyGluIleThr 60
DB 241 GCCGCGCAAGAGCGCCCTCTGGAACCTGCTGCTGCTGCTGAGGGCGAGAGATCC 300
QY 61 PheValSerSerLeuValIlySerSerLeuThrAlaTyrGlnIlyTyrIleTyrIleGlyLeu 80
DB 301 TTCGTGCTCCCTCGTGAAGACATGTAACAGTACTGATGATGATGAGGCTC 360
QY 81 HisAspProSerHisGlyThrLeuProAsnGlySerGlyTyrPylSerSerSerSerAsn 100
DB 361 CATGACCCCAACAGAGGCGACCGACCATGAGAGAGTGGAGTGGAGTGAAGATGAT 420
QY 101 ValLeuThrPheTyrAsnTyrGluArgAsnProSerIleAlaAlaAspArgGlyTyrCys 120
DB 421 GTGATGAATTAATCTTTCATGGAGAGAAATCTCTCCACATCTCAAGCCCGGACATCT 480
QY 121 AlaValLeuSerGlnIlySerGlyPheGlnIlyTyrPylSerPheAsnCysGluAsnGlu 140
DB 481 GCGAGCTGTGAGAGACAGCATTTCTGAGGTGGAAGATTATTAATCTGATATGTGAGG 540

QY 141 LeuProTyrIleCysIlySphe 147
DB 541 TTACCCATGCTGCAAGATTC 561

RESULT 12
US-07-778-156-4
Sequence 4, Application US/07778156
Patent No. 5436169
GENERAL INFORMATION:
APPLICANT: IOVANNA, JUAN-LUCIO
APPLICANT: KEIM, VOLKER
TITLE OF INVENTION: DAGORN, JEAN-CHARLES
TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/778,156
FILING DATE: 19911219
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBION, No. 5436169man F.
REGISTRATION/DOCKET NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 354-012-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEX: 248955 OPAT UR

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 522 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULAR TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: pancreas
US-07-778-156-4

Alignment Scores:
Pred. No.: 6,96e-50 Length: 522
Score: 485.00 Matches: 81
Percent Similarity: 77.40% Conservative: 32
Best Local Similarity: 55.48% Mismatches: 33
Query Match: 59.22% Indels: 0
Gaps: 0
DB:

US-09-659-379-6_COPY_27_175 (1-149) x US-07-778-156-4 (1-522)

QY 1 GluGluSerGlnIlySLeuProSerArgIleThrCysProGlnIlySerValAla 20
DB 79 GAAGAACCCCAAGAGGAACTGCTCGAAGATCCGCTGCCAAGGCTCCAGGCC 138
QY 21 TyrGlySerTyrCysTyrSerLeuIleLeuIleProGlnIlyThrPheSerAlaGluLeu 40
DB 139 TATGGCTCCCACTGATGCTGTTTGTTCACCAAAATCTGGACAGATGAGATCTG 198
QY 41 SerCysGlnMetHisPheSerGlyHisLeuAlaPheLeuSerThrGlyGluIleThr 60

Db 199 GCGTGCAGAGCGCCCTCTGGAACCTGGTGTCTGTCTGCTCAGTGGGCTGAGGATCC 258
QY PheValSerSerLeuValIysAsnSerLeuThrAlaTyrGlnIleTyrIleGlyLeu 30
Db 259 TTCGTCTCTCTCTGTTGAGAGCATTTGTAACAGCTACTCATCTCTGAGATTGGGCTC 318
QY HisAspProSerHisGlyThrLeuProAsnGlySerGlyTyrIleTyrSerSerSerAsn 100
Db 319 CATGACCCACACAGGAGCCAGCCCATGTGAGAAAGTTGGAGTGGAGTACAGTACTGAT 378
QY 101 ValIleuThrPheTyrAsnTyrPgluArganProSerIleAlaAlaAspArgGlyTyrCys 120
Db 379 GGTGATGATTTACTTTCATGAGAGAAATCCCTCCACCATCTCAAGCCCGGACATGT 438
QY 121 AlaValIleuSerGlnIlySerGlyPheGlnIlySTyrPargAspPheAsnGlyAsnGln 140
Db 439 GCGAGCCTGTGAGAGACACAGCATTTTCTGAGGTGAGAAAGTTAATTAATGTGAGG 498
QY 141 LeuProTyrIleCysLys 146
Db 499 TTACCCATGTCTGCATA 516

RESULT 13

US-08-422-166-4

; Sequence 4, Application US/08422166

; Patent No. 5959086

; GENERAL INFORMATION:

; APPLICANT: IOVANNA, JUAN-LUCIO

; APPLICANT: KEIM, VOLKER

; APPLICANT: DAGORN, JEAN-CHARLES

; TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE

; TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

; STREET: 1755 Jefferson Davis Highway, Fourth Floor

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/422,166

; FILING DATE: 14-APR-1995

; CLASSIFICATION: 435

; PRIORITY INFORMATION DATA:

; APPLICATION NUMBER: US 07/778,156

; FILING DATE: 19-DEC-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Oblon, No. 5959086man F.

; REGISTRATION NUMBER: 24,618

; REFERENCE/DOCKET NUMBER: 354-012-0 PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)521-4500

; TELEFAX: (703)486-2347

; TELEEX: 248855 OPAT UR

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 522 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: cDNA

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; TISSUE TYPE: pancreas

; US-08-422-166-4

Alignment Scores:

Pred. No.:	6,96e-50	Length:	522
Score:	485.00	Matches:	81
Percent Similarity:	77.40%	Conservative:	32
Best Local Similarity:	55.48%	Mismatches:	33
Query Match:	59.22%	Indels:	0
DB:	2	Gaps:	0

US-09-659-379-6_COPY_27_175 (1-149) x US-08-422-166-4 (1-522)

QY 1 GlnGluSerGlnIlyLeuProSerSerArgIleThrCysProGlnIlySerValAla 20
Db 79 GAGGAGCCACAGAGGAGCATGCCCTCTGACAGATCCGCTGCCAAGGCTCCAAGGCC 138
QY 21 TyrGlySerTyrCysTyrSerLeuIleLeuIleProGlnIlyTyrSerAsnAlaGlnLeu 40
Db 139 TATGCTCCACTGCTATGCTCTTGTCTTGTCCACCAAAATCCTGGACAGATGCAATCTG 198
QY 41 SerCysGlnMetHisPheSerGlyHisPheAlaPheLeuLeuSerThrGlyGlnIleThr 60
Db 199 GCGTGCAGAGAGCGCCCTCTGGAACCTGTGTCTGTCTGCTGAGGCTGAGGATCC 258
QY 61 PheValSerSerLeuValIysAsnSerLeuThrAlaTyrGlnIlyTyrIleTyrIleGlyLeu 80
Db 259 TTCGTCTCTCTCTGTTGAGAGCATTTGTAACAGTACTCATGCTGTGATTTGGGCTC 318
QY 81 HisAspProSerHisGlyThrLeuProAsnGlySerGlyTyrIlyTyrIleTyrIleTyrCys 100
Db 319 CATGACCCACACAGGAGCATCCAGCCCAATGAGAAAGTTGGAGTGGAGTGAAGCATGTAT 378
QY 101 ValIleuThrPheTyrAsnTyrPgluArganProSerIleAlaAlaAspArgGlyTyrCys 120
Db 379 GGTGATGATTAATTTGATGATGAGAGAAATCCCTCCACCATCTCAAGCCCGGACATGT 438
QY 121 AlaValIleuSerGlnIlySerGlyPheGlnIlySTyrPargAspPheAsnGlyAsnGln 140
Db 439 GCGAGCCTGTGAGAGACACAGCATTTTCTGAGGTGAGAAAGTTAATTAATGTGAGG 498
QY 141 LeuProTyrIleCysLys 146
Db 499 TTACCCATGTCTGCATA 516

RESULT 14

US-08-822-261-2

; Sequence 2, Application US/08822261

; Patent No. 5935813

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: NOVEL HUMAN PANCREATITIS-ASSOCIATED

; TITLE OF INVENTION: PROTEIN

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Inocyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/822,261

; FILING DATE: Filed Herewith

; CLASSIFICATION: 530

; PRIORITY INFORMATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

Mon Aug 9 09:27:51 2004

us-09-659-379-6_copy_27_175.rn1

Page 11

Db 612 TTACCTATGCTGCAAGTTCAAG 635

Search completed: August 8, 2004, 06:58:44
Job time : 82 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 8, 2004, 06:49:57 ; Search time 412 Seconds

(without alignments)
1773.223 Million cell updates/sec

Title: US-09-659-379-6_COPY_27_175

Perfect score: 819
Sequence: 1 EESQKLPSSRITCPQGSVA.....QKMRDNCENELPYICKRV 149

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Ygapop 10.0 ,	Ygapext 0.5
Fgapop 6.0 ,	Fgapext 7.0
Delop 6.0 ,	Delext 7.0

Searched: 3222919 seqs, 245157024 residues

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published Applications NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blomsum62
-TRANS=numan40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptio -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09659379 @CGN 1 1 519 @runat_30072004_175950_21116
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DISPLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:*

1:	/cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
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3:	/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4:	/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5:	/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6:	/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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8:	/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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10:	/cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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13:	/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
14:	/cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
15:	/cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
16:	/cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
17:	/cgn2_6/ptodata/1/pubpna/US10C_NEW_PUB.seq:*
18:	/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
19:	/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	819	100.0	525	17	US-10-231-494-18	Sequence 18, Appl
2	819	100.0	586	9	US-09-739-262-3	Sequence 3, Appl
3	819	100.0	747	16	US-10-421-363-2	Sequence 2, Appl
4	799	97.6	445	17	US-10-231-494-20	Sequence 20, Appl
5	791	96.6	441	17	US-10-231-494-22	Sequence 22, Appl
6	582	71.1	6586	16	US-10-339-767-2	Sequence 23, App
7	520	63.5	781	16	US-10-191-803-235	Sequence 147, App
8	517	63.1	528	12	US-09-997-722-147	Sequence 146, App
9	517	63.1	759	12	US-09-997-722-146	Sequence 37, Appl
10	496	60.6	530	16	US-10-028-268A-37	Sequence 150, App
11	491	60.0	528	12	US-10-107-782-37	Sequence 5, Appl
12	491	60.0	797	15	US-10-316-761-5	Sequence 149, App
13	491	60.0	807	12	US-09-997-722-149	Sequence 171, App
14	491	60.0	940	10	US-10-316-761-2	Sequence 2, Appl
15	491	60.0	940	10	US-09-925-301-171	Sequence 6, Appl
16	485	59.2	762	15	US-10-316-761-6	Sequence 451, App
17	485	59.2	798	9	US-09-978-295A-451	Sequence 451, App
18	485	59.2	798	15	US-10-316-761-6	Sequence 451, App
19	485	59.2	859	9	US-09-978-697-451	Sequence 451, App
20	485	59.2	859	9	US-09-978-192A-451	Sequence 451, App
21	485	59.2	859	9	US-09-978-192A-451	Sequence 451, App
22	485	59.2	859	9	US-09-998-832A-451	Sequence 451, App
23	485	59.2	859	10	US-09-978-189-451	Sequence 451, App
24	485	59.2	859	10	US-09-978-608A-451	Sequence 451, App
25	485	59.2	859	10	US-09-978-585A-451	Sequence 451, App
26	485	59.2	859	10	US-09-978-824-451	Sequence 451, App
27	485	59.2	859	10	US-09-978-403A-451	Sequence 451, App
28	485	59.2	859	10	US-09-978-664A-451	Sequence 451, App
29	485	59.2	859	10	US-09-999-833A-451	Sequence 451, App
30	485	59.2	859	10	US-09-978-193A-451	Sequence 451, App
31	485	59.2	859	10	US-09-981-915A-451	Sequence 451, App
32	485	59.2	859	10	US-09-918-585A-451	Sequence 451, App
33	485	59.2	859	10	US-09-978-423A-451	Sequence 451, App
34	485	59.2	859	10	US-09-978-193A-451	Sequence 451, App
35	485	59.2	859	10	US-09-999-830A-451	Sequence 451, App
36	485	59.2	859	10	US-09-978-187B-451	Sequence 451, App
37	485	59.2	859	10	US-09-978-187B-451	Sequence 451, App
38	485	59.2	859	10	US-09-978-643A-451	Sequence 451, App
39	485	59.2	859	10	US-09-978-375A-451	Sequence 451, App
40	485	59.2	859	10	US-09-978-298A-451	Sequence 451, App
41	485	59.2	859	10	US-09-978-188A-451	Sequence 451, App
42	485	59.2	859	10	US-09-978-188A-451	Sequence 451, App
43	485	59.2	859	10	US-09-978-194A-451	Sequence 451, App
44	485	59.2	859	10	US-09-999-829A-451	Sequence 451, App
45	485	59.2	859	10	US-09-978-299A-451	Sequence 451, App

ALIGNMENTS

RESULT 1
US-10-231-494-18
Sequence 18, Application US/10231494
Publication No. US2004002334A1
GENERAL INFORMATION:
APPLICANT: Prior, Christopher P.
FILE OF INVENTION: Modified Transferrin Fusion Proteins
TITLE REFERENCE: 54710-5001-US
CURRENT APPLICATION NUMBER: US/10/231,494
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 60/315,745
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: US 60/334,059
PRIOR FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 525
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: INGP
OTHER INFORMATION: sequences

FEATURE:
NAME/KEY: CDS
LOCATION: (1) ... (525)
US-10-231-494-18

Alignment Scores:

Pred. No.: 4.44e-101 Length: 525
Score: 819.00 Matches: 149
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-659-379-6_COPY_27_175 (1-149) x US-10-231-494-18 (1-525)

QY 1 GUGLUSERGILNLYSLLEUPROSERARGLIETHRCYSPROGILGYSERVALA 20
DB 79 GAAGATCTCAAAAAAATGGCATCTCTAGAAATTACTTGCACAAAGTTCTGTGCT 138
QY 21 TYRGLYSERTYRCYTSERILEULEULEIPROGINHTRTPSERASNAIGLULEU 40
DB 139 TATGGTCTTATTTGATTTCTTGAATTTGATTCACAAACTGGCTTATCTGATTTG 198
QY 41 SERCYGINMETHISPHESERGLYHISLEUALAPHELEUSERTHRGILGILUETHR 60
DB 199 TCTTGCAATCATTTTCTGCTCATTTGGCTTTTCTTCTGCTGATGAAATTACT 258
QY 61 PHEVALSERSELEUVALYASNSERLEUTHRALATYRGILUETHR 80
DB 259 TTGTTCTCTCTTGGTTAAATAATCTTGACCTGCTTCAATATATTGGAATGGTTTG 318
QY 81 HISAPPROSERHISGLYTHLEUPROANGLYSERGLYTPLYSTPSESERSEN 100
DB 319 CATGATCCATCATCATGACTTGGCCAAATGGTTGGTGGAAAGCTTCTTAT 378
QY 101 VALLEUTHRPHETYSANTTPGLUARGANPROSERILEALALASPARGLYTYRCYS 120
DB 379 GTTTTACCTTTTATATTTGGAAAGAAATCCATATTGCTGCTGATGAGGTTATGT 438
QY 121 ALAVALLEUSERGILNLYSERGLYPHEGILNLYSTPARGASPHEANCYSGILUANGILU 140
DB 439 GCGTTTGTCTCAAAATCTGGTTTCAAAAATGAGAGATTTAATGTGAAAAATGAA 498
QY 141 LEUPROTYRILECYSLYSPHELYSVAL 149
DB 499 TTGCCATATATTGTAAATTTAAAGTT 525

RESULT 2

US-09-739-262-3

Sequence 3, Application US/09739262
Patent No. US2002003167A1
GENERAL INFORMATION:
APPLICANT: Dieckgraefe, Brian K.
TITLE OF INVENTION: Gene Markers for Chronic Mucosal Injury
FILE REFERENCE: 04255,75314
CURRENT APPLICATION NUMBER: US/09/739,262
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 09/146,969
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 586
TYPE: DNA
ORGANISM: Homo sapiens
US-09-739-262-3

Alignment Scores:
Pred. No.: 5.22e-101 Length: 586
Score: 819.00 Matches: 149
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-09-659-379-6_COPY_27_175 (1-149) x US-09-739-262-3 (1-586)

QY 1 GUGLUSERGILNLYSLLEUPROSERARGLIETHRCYSPROGILGYSERVALA 20
DB 72 GAAGATCTCAAAAAAATGGCATCTCTAGAAATTACTTGCACAAAGTTCTGTGCT 131
QY 21 TYRGLYSERTYRCYTSERILEULEULEIPROGINHTRTPSERASNAIGLULEU 40
DB 132 TATGGTCTTATTTGATTTCTTGAATTTGATTCACAAACTGGCTTATCTGATTTG 191
QY 41 SERCYGINMETHISPHESERGLYHISLEUALAPHELEUSERTHRGILGILUETHR 60
DB 192 TCTTGCCATGATGCAATTTCTTCCAGACCTGGCATTTCTTCCAGTACCTGGGAAATTACC 251
QY 61 PHEVALSERSELEUVALYASNSERLEUTHRALATYRGILUETHR 80
DB 252 TTGTTCTCTCTTGGTTAAATAATCTTGACCTGCTTCAATATATTGGAATGGTTTG 311
QY 81 HISAPPROSERHISGLYTHLEUPROANGLYSERGLYTPLYSTPSESERSEN 100
DB 312 CATGATCCCTCAATGATGACTACCAACGGAAGTGATGGAAGTGAGCGATTCAT 371
QY 101 VALLEUTHRPHETYSANTTPGLUARGANPROSERILEALALASPARGLYTYRCYS 120
DB 372 GTGCTGACCTTCTATTAATCTGGAGAGAACTCTTATTTGCTGATGAGGTTATGT 431
QY 121 ALAVALLEUSERGILNLYSERGLYPHEGILNLYSTPARGASPHEANCYSGILUANGILU 140
DB 432 GCGTTTGTCTCAAAATCTGGTTTCAAAAATGAGAGATTTAATGTGAAAAATGAG 491
QY 141 LEUPROTYRILECYSLYSPHELYSVAL 149
DB 492 CTTCCATATATCTGCAAAATTTCAAGTTC 518

RESULT 3

US-10-421-363-2

Sequence 2, Application US/10421363
Publication No. US20040018623A1
GENERAL INFORMATION:
APPLICANT: Rosenberg, Lawrence
TITLE OF INVENTION: MEDIUM FOR PREPARING DIFFERENTIATED
FILE REFERENCE: 701826-05621-CIP
CURRENT APPLICATION NUMBER: US/10/421,363
CURRENT FILING DATE: 2003-04-23
PRIOR APPLICATION NUMBER: US 10/111,485
PRIOR FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: PCT/CA00/01284
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/162,137
PRIOR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 747
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Mammalian INGAP
FEATURE:
NAME/KEY: CDS
LOCATION: (20) ... (541)
US-10-421-363-2

Alignment Scores:
Pred. No.: 7.49e-101 Length: 747
Score: 819.00 Matches: 149
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-09-659-379-6_COPY_27_175 (1-149) x US-10-421-363-2 (1-747)

QY 1 GlnGluSerGlnLysLeuProSerSerArgIleThrCysProGlnGlySerValAla 20
 Db 95 GAGAAATCTCAAAAGAAAGTGCCTTCTTCACTATTAACCTGCTCAAGGCTCTGACCC 154
 QY 21 TTTGlySerTyrCysTyrSerLeuIleLeuIleProGlnIleThrTyrSerAsnAlaGluLeu 40
 Db 155 TATGGGTCTCTATTTGCTATCTACTGATTTTGATACCAAGACCTGGCTTAATGCAAGACTA 214
 QY 41 SerCysGlnMetHisPheSerGlyHisLeuAlaPheLeuLeuSerThrGlyGluIleThr 50
 Db 215 TCTGGCCAGATGCAATTTCTCAGGACACCTGGGATTTCTTCTCAGTACCTGGTGAATTACC 274
 QY 61 PheValSerSerLeuValLysAsnSerLeuThrAlaTyrGlnIleTyrIleTyrIleGlyLeu 30
 Db 275 TTGGGTCTCTCTCTTGTAAAGACGTTTGACGGCTTACCACTGATCATCTGATTTGACCTC 334
 QY 81 HisAspProSerHisGlyThrLeuProAsnGlySerGlyTyrProLysTyrSerSerAsn 100
 Db 335 CATATCCCTCACTGACACTGACCTACCCACGAAAGTGAATGAGATGAGAGCAAGTTCCAT 394
 QY 101 ValLeuThrPheTyrAsnTyrGluArgAsnProSerIleAlaAlaAspArgGlyTyrCys 120
 Db 395 GTGCTGACCTTCTATTAAGTGGAGAGGAACTCTCTATTTGCTGACCTGGTATTATGT 454
 QY 121 AlaValLeuSerGlnLysSerGlyPheGlnLysTyrPargAspPheAsnGluAsnGlu 140
 Db 455 GCAGTTTGTCTCGAAGATCGGTTTTCAGAAAGTGAGAGATTTAATGTGAAAGATGAG 514
 QY 141 LeuProTyrIleCysLysPheLysVal 149
 Db 515 CTTCCCTATATCTGCAATTCAGAGTC 541

RESULT 4

US-10-231-494-20
 ; Sequence 20, Application US/10231494
 ; Publication No. US2004002334A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Prior, Christopher P.
 ; TITLE OF INVENTION: Modified Transferrin Fusion Proteins
 ; FILE REFERENCE: 54710-5001-US
 ; CURRENT APPLICATION NUMBER: US/10/231,494
 ; CURRENT FILING DATE: 2002-08-30
 ; PRIOR APPLICATION NUMBER: US 60/315,745
 ; PRIOR FILING DATE: 2001-08-30
 ; PRIOR APPLICATION NUMBER: US 60/334,059
 ; PRIOR FILING DATE: 2001-11-30
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 20
 ; LENGTH: 445
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: IN GAP
 ; OTHER INFORMATION: sequences for fusion proteins
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(444)
 ; US-10-231-494-20

Alignment Scores:

Pred. No.: 1,799-98 Length: 445
 Score: 799.00 Matches: 144
 Percent Similarity: 100.00% Conservative: 2
 Best Local Similarity: 98.63% Mismatches: 0
 Query Match: 97.56% Indels: 0
 DB: 17 Gaps: 0

US-09-659-379-6_COPY_27_175 (1-149) x US-10-231-494-20 (1-445)

QY 4 GlnLysLysLeuProSerSerArgIleThrCysProGlnGlySerValAlaTyrGlySer 23
 Db 4 GAGAAAGCTTCCATCTTCCAGAAATTAATCTGTCACCAAGGTTCTGTTAGTTCT 63
 QY 24 TyrCysTyrSerLeuIleLeuIleProGlnIleThrTyrSerAsnAlaGluLeuSerGln 43
 Db 64 TATGTTATTTGATTTGATTTATTCACAACTGGTCTAATGCGAATGCTTGTGTCAA 123
 QY 44 MethiPheSerGlyHisLeuAlaPheLeuLeuSerThrGlyGluIleThrPheValSer 63
 Db 124 ATGATTTTCTGGTCATTTGGCTTTTGTGTCTACTGATGGAATTAATCTTGTCT 183
 QY 64 SerLeuValLysAsnSerLeuThrAlaTyrGlnIleTyrIleTyrIleGlyLeuHisAspPro 83
 Db 184 TCTTGGTTAAATAATCTTGTACGCTTATCAATATATTTGATTTGATTTGATATCA 243
 QY 84 SerHisGlyThrLeuProAsnGlySerGlyTyrProLysTyrSerSerAsnValLeuThr 103
 Db 244 TCTATGTTACTTTGCGAATGTTCTGGTGGAAATGTTCTTCTCAATGTTTGAAT 303
 QY 104 PheTyrAsnTyrGluArgAsnProSerIleAlaAlaAspArgGlyTyrCysAlaValLeu 123
 Db 304 TTTTACAAATTCGGAAGAAATCCATCTATCTCTGCTATAGAGTTATTTGCTGTTTG 363
 QY 124 SerGlnLysSerGlyPheGlnLysTyrPargAspPheAsnGluAsnGluLeuProTyr 143
 Db 364 TCTCAAAATCTGTTTTCAAAATGAGAGATTTAATGTGAAAATGAAATGCAATAT 423
 QY 144 IleCysLysPheLysVal 149
 Db 424 ATTGTAAATTTTAAAGTT 441

RESULT 5

US-10-231-494-22
 ; Sequence 22, Application US/10231494
 ; Publication No. US2004002334A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Prior, Christopher P.
 ; TITLE OF INVENTION: Modified Transferrin Fusion Proteins
 ; FILE REFERENCE: 54710-5001-US
 ; CURRENT APPLICATION NUMBER: US/10/231,494
 ; CURRENT FILING DATE: 2002-08-30
 ; PRIOR APPLICATION NUMBER: US 60/315,745
 ; PRIOR FILING DATE: 2001-08-30
 ; PRIOR APPLICATION NUMBER: US 60/334,059
 ; PRIOR FILING DATE: 2001-11-30
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 22
 ; LENGTH: 441
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: IN GAP
 ; OTHER INFORMATION: sequences for fusion proteins
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (2)..(436)
 ; US-10-231-494-22

Alignment Scores:

Pred. No.: 2,150-97 Length: 441
 Score: 791.00 Matches: 143
 Percent Similarity: 99.31% Conservative: 1
 Best Local Similarity: 98.62% Mismatches: 1
 Query Match: 96.58% Indels: 0
 DB: 17 Gaps: 0

US-09-659-379-6_COPY_27_175 (1-149) x US-10-231-494-22 (1-441)

QY 5 LysLysLeuProSerSerArgIleThrCysProGlnGlySerValAlaTyrGlySerTyr 24
 Db 2 CGACCTTGCATCTTCCAGAAATTAATCTGTCACCAAGGTTCTGTTGATTTAT 61

QY 25 CysTyrSerLeuIleLeuIleProGlnThrTyrSerAsnAlaGluLeuSerCysGlnMet 44
DB 62 TGTATTCTTGTGATTGATCCCAAACTGCTGTAATGCTGAATGCTTGTCAATG 121
QY 45 HisPheSerGlyHisIleuAlaPheLeuLeuSerThrGlyGluIleThrPheValSerSer 64
DB 122 CATTTTCTGCTGCTATTTGGCTTTTGTGCTACTGCTGAATTAATCTTTGTTCTTCT 181
QY 65 LeuValIlyAsnSerLeuThrAlaTyrGlnTyrIleThrIleGlyLeuHisAspProSer 84
DB 182 TTGTTTAAAAATCTTTGACAGCTGATCATATATTTGATGTTGTTGCATGATCCATCT 241
QY 85 HisGlyThrLeuProAsnGlySerGlyTyrIlyStrPseSerSerAsnValLeuThrPhe 104
DB 242 CATGTTACTTGGCCAAATGTTGCTGTTGGAATGCTTCTTCTAAATGTTTGACTTTT 301
QY 105 TyrAsnTrpGluArgAsnProSerIleAlaIleAspArgGlyTyrCysAlaValLeuSer 124
DB 302 TACAAATGGGAAAGAAATCCATCTATTGCTGCTGATTAAGTTATGCTGTTTGTCT 361
QY 125 GlnIlySerGlyPheGlnIlyStrPargAspPheAsnGlyIlyAsnGluLeuProTyrIle 144
DB 362 CAAAATCTGTTTCAAAATGAGAGATTTTAATGTGAATGAATGCAATGCTATATAT 421
QY 145 CysIlyPheIlyVal 149
DB 422 TGTAAATTTAAAGTT 436

RESULT 6

US-10-339-767-2
Sequence 2, Application US/10339767
Publication No. US20030207301A1
GENERAL INFORMATION:
APPLICANT: GMP Endotherapeutics, Inc.
APPLICANT: Taylor-Fishwick, David A
APPLICANT: Vinik, Aaron I
TITLE OF INVENTION: Assay for the Detection of Factors that Modulate the Expression
FILE REFERENCE: 9061X#L5
CURRENT APPLICATION NUMBER: US/10/339,767
CURRENT FILING DATE: 2003-01-09
PRIOR APPLICATION NUMBER: US 60/388,315
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: US 60/361,073
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/346,898
PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 6586
TYPE: DNA
ORGANISM: Hamster sp.
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(6586)
OTHER INFORMATION: n = A, C, G, or T
US-10-339-767-2

Alignment Scores:

Pred. No.: 2, 62e-67 Length: 6586
Score: 582.00 Matches: 148
Percent Similarity: 30.27% Conservative: 0
Best Local Similarity: 30.27% Mismatches: 1
Query Match: 71.06% Indels: 341
Gaps: 3

US-09-659-379-6_COPY_27_175 (1-149) x US-10-339-767-2 (1-6586)

QY 1 GlnGluSerGlnIlyStrPseSerArgIleThrCysProGlnGlySerValAla 20
DB 4445 GAAGAAATCTCAAAAGAAATGCTTCTTCAAGTAAATGCTGCTCAAGGCTGTGAGCC 4504

QY 21 TyrGlySerTyrCysTyrSerLeuIleLeuIleProGlnThrTyrSerAsnAlaGlu--- 39
DB 4505 TATGGGTCCTATTGCTATTCTACATGATTTTATACACAGACCTGCTTAATGAGAAAGTG 4564
QY 39 ----- 39
DB 4565 AGTAGACACACACAGATGGGAAATAGAAACAGAACTTCCGGGCTCAAGAGTGCTGT 4624
QY 39 ----- 39
DB 4625 TGGATTCAATCTCTGTGTTATTATGACTGAGTGGAACCAATCCCTCACCTACACTCT 4684
QY 40 -----LeuSerCys 42
DB 4685 ACCACTCCAGTGGGGTTAATATGTTTCCATTCTGCTCTTCAAAACAGCTATCTGCG 4744
QY 43 GlnMetHisPheSerGlyHisIleuAlaPheLeuLeuSerThrGlyGluIleThrPheVal 62
DB 4745 CAGATGCAATTTCTCAGACACCTGCACTTCTCTCAGTACTGCTGAATTAATCTGCTG 4804
QY 63 SerSerLeuValIlyAsnSerLeuThrAlaTyrGlnTyrIleThrIleGlyLeuHisAsp 82
DB 4805 TCCTCCCTTGTGAAGAAACAGTTTGACGGCCTACAGTACATCTGGAATTGCACTCATGAT 4864
QY ProSerHis----- 85
DB 4865 CCTTCACATGTGCGATCCTATCTTGTCTGCTTTTCTCTCATAGTCCCTTTATCCCTG 4924
QY 85 ----- 85
DB 4925 TGAAGATTCCTGTGACACCCAGAAAGCAAAATGGGTCATAGATCTCCAATGCTGGA 4984
QY 85 ----- 85
DB 4985 TGGCATTTAGAGAGAGGAAATATCATGCTGATAGATTAAGTTCTGTGAATCTCAGAGTT 5044
QY 85 ----- 85
DB 5045 CAGTTGAAGTCTGTATGCTATGCTGACTTCTTAAGTTTCTATGAGATATTGGAAGAT 5104
QY 85 ----- 85
DB 5105 AATTATCATCATGTTTAGGAGTCTGCAATATACAGTGCATTAATGCTGAACAAAGAA 5164
QY 85 ----- 85
DB 5165 TCTTTTGTGTTTTTCTCTTATAGAAATAGATTTTGTTCAGTGTGTTCTGAGAAACCTGA 5224
QY 85 ----- 85
DB 5225 AAAGTACACCAATTGTATTTATCAGAACTGATAAATCCAGTAATCCCAATTTCATT 5284
QY 85 ----- 85
DB 5285 CCATAGTTTCTGGGGGTTGTAAATAGACGTAGATTTCTGGGATAATATTACACAGA 5344
QY 85 ----- 85
DB 5345 AGGCTTTTGGCAATGGGTATGACCATACCAAGTTGTAAAGCTAGGACGGACCAAA 5404
QY 86 -----GlyThr 87
DB 5405 TGTTCAGTGAAGTATCATGTAATCTGTAACCAATCTTTGCACTNTTACAGGTTAC 5464
QY 87 rLeuProAsnGlySerGlyTyrIlyStrPseSerSerAsnValIleuThrPheTyrAsnTr 107
DB 5465 ACTAACCCACGGAAGTGTGAGAGTGAACAGTTCCAATGTGCTGCTCTTCTATTAATCTG 5524
QY 107 pGluArgAsnProSerIleAlaIleAspArgGlyTyrCysAlaValLeuSerGlnIlySse 127
DB 5525 GGAAGAGAAACCCCTCTATGCTGCTGACCGGTGTTATTGTGCAAGTTTGTCTCAGAAATC 5584

Qy 127 r----- 127
Db 5585 -AGGTAGACAGAGAAACCACTGTGATTAAACCATCTTCCACATCCAGTATGACA 5643
Qy 127 ----- 127
Db 5644 COTGGGCTGACAGAGTTTGAGACATACAGTGTGAGCGTGTGTTGTCTCTCTC 5703
Qy 127 ----- 127
Db 5704 ATGTTGCTTATATGTCTCTTGCACAGATTTATCATGCAGAAAGATGCTTAAGTC 5763
Qy 127 ----- 127
Db 5764 AAGAGACAGACAGTACATCTTTGTTGAGTTCACAGATTCACCTGCCCATCTT 5823
Qy 128 ----- 141
Db 5824 TACCTCTATCTCTCTGTGAGTTTTCAGAGTGGAGATTTTAAATGAGCT 5883
Qy 141 uProtyrilleCyslyspheylsVal 149
Db 5884 TCCTATATCTGCAAAATTCAGATC 5908

RESULT 7

US-10-191-803-235
; Sequence 235, Application US/10191803
; Publication No. US20040014040A1
; GENERAL INFORMATION:
; APPLICANT: MENDRICK, Donna
; APPLICANT: PORTER, Mark
; APPLICANT: JOHNSON, Kory
; APPLICANT: HIGGS, Brandon
; APPLICANT: CASTLE, Arthur
; APPLICANT: ELASHOFF, Michael
; TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5090US
; CURRENT APPLICATION NUMBER: US/10/191,803
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/303,819
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/305,623
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/369,351
; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: US 60/377,611
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 1140
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 235
; LENGTH: 781
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20040014040A1 NM_053289
US-10-191-803-235

Alignment Scores:

Pred. No.: 2,846-60 Length: 781
Score: 520.00 Matches: 86
Percent Similarity: 78.23% Conservative: 29
Best Local Similarity: 58.50% Mismatches: 32
Query Match: 63.49% Indels: 0
DB: 16 Gaps: 0

US-09-659-379-6_COPY_27_175 (1-149) x US-10-191-803-235 (1-781)

Qy 1 GluGluSerGlnIlyLeuProSerSerArgIleThrCysProGlnGlySerValAla 20
Db 138 GAAGACTCTCCGAAAGAAATACCTCTGACGCAATTAAGTCCCAAGGCTCCAGGCA 197
Qy 21 TyrGlySerTyrCysTyrSerLeuIleLeuIleProGlnThrTyrSerAsnAlaGluLeu 40

Db 198 TATGCTCTACTGCTATAGCCCTGTTCAGATACCAAGACCTGGTTGATGACGAAGCTG 257
Qy 41 SerCysGlnMetHisPheSerGlyHisLeuAlaPheLeuLeuSerThrGlyIleLeuThr 60
Db 258 GCTGCGCAGAGAGACCTGGAACACCTTGATCTGTGCTCAATGATGAGCTTCA 317
Qy 61 PheValSerSerLeuValIlyAsnSerLeuThrAlaTyrGlnTyrIleTyrIleGlyLeu 80
Db 318 TCTTGCAATCCATGCTGCAAGAACACTGGAACAGCTTACCAATATCTGATTTGACTC 377
Qy 81 HisAspProSerHisGlyThrLeuProAsnGlySerGlyTyrIlyPheSerSerSerAsn 100
Db 378 CATGACCCACTCTGTGGTGGAGAACCAATGAGAGTGGATGGATGAGTAAATGAC 437
Qy 101 ValLeuThrPheTyrAsnTyrGlnIlyAsnProSerIleAlaAlaAspArgGlyTyrCys 120
Db 438 AATATGATTAATATGCAACTGGAGAGAACCAATCTCTGCTTAAAGCCGGGATCTCTGT 497
Qy 121 AlaValLeuSerGlnIlySerGlyPheGlnIlySerTyrPheAspPheAsnCysGlyAsnGly 140
Db 498 GGCAGCTTGTCAAGATCTCTGAGTTTCTTAAGATGAGAGATACCAATGTAAGTGAAG 557
Qy 141 LeuProTyrIleCysIlysphe 147
Db 558 TTGCCCTACGCTCCAAATTT 578

RESULT 8

US-09-997-722-147
; Sequence 147, Application US/09997722
; Publication No. US20040072154A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71171/RMS/DCF
; CURRENT APPLICATION NUMBER: US/09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 147
; LENGTH: 528
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-997-722-147

Alignment Scores:

Pred. No.: 4,056-60 Length: 528
Score: 517.00 Matches: 86
Percent Similarity: 77.55% Conservative: 28
Best Local Similarity: 58.50% Mismatches: 33
Query Match: 63.13% Indels: 0
DB: 12 Gaps: 0

US-09-659-379-6_COPY_27_175 (1-149) x US-09-997-722-147 (1-528)

Qy 1 GluGluSerGlnIlyLeuProSerSerArgIleThrCysProGlnGlySerValAla 20
Db 79 GAAGACTCTCCGAAAGAAATACCTCTGACGCAATTAAGTCCCAAGGCTCCAGGCT 138
Qy 21 TyrGlySerTyrCysTyrSerLeuIleLeuIleProGlnThrTyrSerAsnAlaGluLeu 40
Db 139 TATGCTCTACTGCTATAGCCCTGTTCAGATACCAAGACCTGGTTGATGCAAGACTG 198
Qy 41 SerCysGlnMetHisPheSerGlyHisLeuAlaPheLeuLeuSerThrGlyIleLeuThr 60
Db 199 GCTGCGCAGAGAGGCTGGAGAGACCTCGATATGTGCTCAATAGCGCTGAGGCTTCA 258
Qy 61 PheValSerSerLeuValIlyAsnSerLeuThrAlaTyrGlnTyrIleTyrIleGlyLeu 80

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Db      259 TTCTTGCTCCATGAGTGAAGACAGAAACAGCTACCATCATCTTGATTTGGGCTC 318
Qy      81 HIASPPROSERHISGLYTHRLEUPROAHNGLYSERGLYTRPLYSRTPSESRERAA 100
Db      319 CAGGACCCCACTCTGGGTGAGAACCCCAATGGAGGTGATGGAGAAAGGAGTAACAATGAC 378
Qy      101 ValLeuThPhetYrAnTrpGluArgAsnProSerIleAlaAlaSpApgGlyYrCys 120
Db      379 GTGATGAATTACTTTAACTTGGAGAGAACCCATCTACTGCTTAAGACCTGCTTCTGT 438
Qy      121 AlaValLeuSerGlnLysSerGlyPheGlnLysTrpArgAspPheAsnCysGluAanglu 140
Db      439 GGCAGCTTGCAAGACTTCTGTGATTTCTTAATATGAGAGATATGACATGTAGGTGAAG 498
Qy      141 LeuProTyrIleCysLysPhe 147
Db      499 TTGCCCTATGTCTGCAAAATT 519

RESULT 9
US-09-997-722-146
; Sequence 146, Application US/09997722
; Publication No. US2004007215A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71171/RMS/DCP
; CURRENT APPLICATION NUMBER: US/09/997,722
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 146
; LENGTH: 759
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-997-722-146

Alignment Scores:
Pred. No.: 6,94e-60 Length: 759
Score: 517.00 Matches: 86
Percent Similarity: 77.55% Conservative: 28
Best Local Similarity: 58.50% Mismatches: 33
Query Match: 63.13% Indels: 0
DB: 12 Gaps: 0

US-09-659-379-6_COPY_27_175 (1-149) x US-09-997-722-146 (1-759)
Qy      1 GlnGluSerGlnLysLysLeuProSerSerArgIleThCysProGlnGlySerValAla 20
Db      110 GAAGACTCCCTGAGAGATATACCTCCGACGCGATTAGTGGCCCAAGGCTCCAGGCT 169
Qy      21 TYRGLYSerTyrCysTrpSerLeuIleLeuIleProGlnThrTrpSerAsnAlaGluLeu 40
Db      170 TATGGCTCTCACTGATGCTTGTTCATGATCCACAAGCCTGGTTGATGAGAACTG 229
Qy      41 SerCysGlnMetHisPheSerGlyHisLeuAlaPheLeuLeuSerThrGlyIleIleThr 60
Db      230 GCCTGCCAAAGAGGCTGGAGGACACCTGATCTGTGCTCAATAGCGCTGAGGCTTCA 289
Qy      61 PheValSerSerIleValLysAsnSerLeuThrAlaTyrGlnThrIleTrpIleGlyLeu 80
Db      290 TTCTTCTCTCCATGGGTGAAGAGACAGAAACAGCTACCAATACTTGATTTGGGCTC 349
Qy      81 HIASPPROSERHISGLYTHRLEUPROAHNGLYSERGLYTRPLYSRTPSESRERAA 100
Db      350 CATTGACCCCACTGTGGTGTGAGAACCCCAATGGAGGTGATGGAGTAACAATGAC 409
Qy      101 ValLeuThPhetYrAnTrpGluArgAsnProSerIleAlaAlaSpApgGlyYrCys 120

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Db      410 GTGATGAATTACTTTAACTTGGAGAGAACCCATCTACTGCTTAAGACGCTTCTGT 469
Qy      121 AlaValLeuSerGlnLysSerGlyPheGlnLysTrpArgAspPheAsnCysGluAanglu 140
Db      470 GGCAGCTTGCAAGACTTCTGTGATTTCTTAATATGAGAGATATGACATGTAGGTGAAG 529
Qy      141 LeuProTyrIleCysLysPhe 147
Db      530 TTGCCCTATGTCTGCAAAATT 550

RESULT 10
US-10-028-248A-37
; Sequence 37, Application US/10028248A
; Publication No. US20030235882A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard
; APPLICANT: Patnurajan, Meera
; APPLICANT: Vernet, Corine
; APPLICANT: Casman, Stacie
; APPLICANT: Malvankar, Uriel
; APPLICANT: Shenoy, Suresh
; APPLICANT: Spytek, Kimberly
; APPLICANT: Gangolli, Esha
; APPLICANT: Miller, Charles
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Smithson, Glenda
; APPLICANT: Zerkhusen, Bryan
; APPLICANT: Liu, Xiaohong
; APPLICANT: Colman, Steven
; APPLICANT: Tchernev, Velizar
; APPLICANT: Si, Jingsheng
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Sciore, Paul
; APPLICANT: Millet, Isabelle
; APPLICANT: Rothenberg, Mark
; TITLE OF INVENTION: NO. US20030235882A1el Nucleic Acids and Polypeptides and Methods
; FILE REFERENCE: 21402-222
; CURRENT APPLICATION NUMBER: US/10/028,248A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256619
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/262959
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/272408
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/285189
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/308039
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/311266
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-028-248A-37

Alignment Scores:
Pred. No.: 2,87e-57 Length: 530
Score: 496.00 Matches: 83
Percent Similarity: 77.70% Conservative: 32
Best Local Similarity: 56.08% Mismatches: 33
Query Match: 60.56% Indels: 0
DB: 16 Gaps: 0

US-09-659-379-6_COPY_27_175 (1-149) x US-10-028-248A-37 (1-530)

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QY 1 GluGlnSerGlnValLeuProSerSerArgIleThrCysProGlnGlySerValAla 20
Db 69 GAAAGAACCCCAAGGAGAACTGCTCTGACGAGATCCGCTGCCAAAGGCTCCAAAGGCC 128
QY 21 TyrGlySerTyrCysTyrSerLeuIleLeuIleProGlnThrTyrSerAsnAlaGluLeu 40
Db 129 TATGCTCCCACTGCTATGCGCTGTTTGTTCACCAAAATCTGACAGATGACAGATCTG 188
QY 41 SerCysGlnMetHisPheSerGlyHisLeuAlaPheLeuLeuSerThrGlyGluIleThr 50
Db 189 GCGTCCCAAGGAGCGGCTCTGGAACCTGGTGTCTGTGCTGACGTGGGGCTGAGGATCC 248
QY 61 PheValSerSerLeuValLeuAsnSerLeuThrAlaTyrGlnTyrIleTyrIleGlyLeu 30
Db 249 TTGCTGCTCCCTCCGTAAGAGCATTTGTAACAGCTACTCATACGTGTGATTTGGGCTC 308
QY 81 HisAspProSerHisGlyThrLeuProAsnGlySerGlyTyrIleTyrIleSerSerAsn 100
Db 309 CATGACCCCAACAGGAGGACCGGACCCCAATGAGAGAGTTGGAGGTGAGATGACATGAT 368
QY 101 ValLeuThrPheTyrAsnTyrGlnArgAsnProSerIleAlaAlaAspArgGlyTyrCys 120
Db 369 GTGATGATTAATCTTGTGATGAGAGAAATCCCTCCACCATCTCAAGCCCGGCGCATGT 428
QY 121 AlaValLeuSerGlnValSerGlyPheGlnIleTyrPheAspPheAsnGlyGluAsnGlu 140
Db 429 GCGAGCTGTGTGAGAGACAGCATTTCTGAGGTGAGAAAGATTAATCTGATGTGAGG 488
QY 141 LeuProTyrIleCysIlePheLeu 148
Db 489 TTACCTATGCTGTGCAAGTTCAAA 512
RESULT 11
US-10-107-782-37
; Sequence 37, Application US/10107782
; Publication No. US20040018970A1
; GENERAL INFORMATION:
; APPLICANT: Bolidog, Ferenc,
; APPLICANT: Caeman, Stacie
; APPLICANT: Colman, Steve,
; APPLICANT: Edinger, Shlomit,
; APPLICANT: Gangolli, Esna,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Li, Li,
; APPLICANT: Liu, Xiaohong,
; APPLICANT: Malpankar, Uriel,
; APPLICANT: Miller, Charles,
; APPLICANT: Miller, Isabelle,
; APPLICANT: Patturajan, Meera,
; APPLICANT: Rothenberg, Mark,
; APPLICANT: Sciore, Paul,
; APPLICANT: Shenoy, Suresh,
; APPLICANT: Shinkets, Richard,
; APPLICANT: Si, Jingsheng,
; APPLICANT: Smithson, Glenda,
; APPLICANT: Spytek, Kimberly,
; APPLICANT: Stone, David,
; APPLICANT: Tsupler, Raymond, Jr.,
; APPLICANT: Tchernev, Velizar,
; APPLICANT: Vernet, Corine,
; APPLICANT: Zethusen, Brian
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: 21402-222CIP
; CURRENT APPLICATION NUMBER: US/10107,782
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 10/028,248
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256,619
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/262,959
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/272,408
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; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/285,189
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/308,039
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/311,266
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/279,344
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 37
; LENGTH: 530
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(527)
US-10-107-782-37
Alignment Scores:
Pred. No.: 2,87e-57 Length: 530
Score: 496.00 Matches: 83
Percent Similarity: 77.70% Conservative: 32
Best Local Similarity: 56.08% Mismatches: 33
Query Match: 60.56% Indels: 0
Gaps: 0
US-09-659-379-6_COPY_27_175 (1-149) x US-10-107-782-37 (1-530)
QY 1 GluGlnSerGlnValLeuProSerSerArgIleThrCysProGlnGlySerValAla 20
Db 69 GAAAGAACCCCAAGGAGAACTGCTCTGACGAGATCCGCTGCCAAAGGCTCCAAAGGCC 128
QY 21 TyrGlySerTyrCysTyrSerLeuIleLeuIleProGlnThrTyrSerAsnAlaGluLeu 40
Db 129 TATGCTCCCACTGCTATGCGCTGTTTGTTCACCAAAATCTGACAGATGACAGATCTG 188
QY 41 SerCysGlnMetHisPheSerGlyHisLeuAlaPheLeuLeuSerThrGlyGluIleThr 60
Db 189 GCGTCCCAAGGAGCGGCTCTGGAACCTGGTGTCTGTGCTGACGTGGGGCTGAGGATCC 248
QY 61 PheValSerSerLeuValLeuAsnSerLeuThrAlaTyrGlnTyrIleTyrIleGlyLeu 80
Db 249 TTGCTGCTCCCTCCGTAAGAGCATTTGTAACAGCTACTCATACGTGTGATTTGGGCTC 308
QY 81 HisAspProSerHisGlyThrLeuProAsnGlySerGlyTyrIleTyrIleSerSerAsn 100
Db 309 CATGACCCCAACAGGAGGACCGGACCCCAATGAGAGAGTTGGAGGTGAGATGACATGAT 368
QY 101 ValLeuThrPheTyrAsnTyrGlnArgAsnProSerIleAlaAlaAspArgGlyTyrCys 120
Db 369 GTGATGATTAATCTTGTGATGAGAGAAATCCCTCCACCATCTCAAGCCCGGCGCATGT 428
QY 121 AlaValLeuSerGlnValSerGlyPheGlnIleTyrPheAspPheAsnGlyGluAsnGlu 140
Db 429 GCGAGCTGTGTGAGAGACAGCATTTCTGAGGTGAGAAAGATTAATCTGATGTGAGG 488
QY 141 LeuProTyrIleCysIlePheLeu 148
Db 489 TTACCTATGCTGTGCAAGTTCAAA 512
RESULT 12
US-09-997-722-150
; Sequence 150, Application US/09997722
; Publication No. US20040072154A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71171/RMS/DCF
; CURRENT APPLICATION NUMBER: US/09/997,722
; CURRENT FILING DATE: 2001-11-30
```

PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 301
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 150
LENGTH: 528
TYPE: DNA
ORGANISM: Homo sapiens
US-09-997-722-150

Alignment Scores:
Pred. No.: 1,366-56 Length: 528
Score: 491.00 Matches: 82
Percent Similarity: 77.55% Conservative: 32
Best Local Similarity: 55.78% Mismatches: 33
Query Match: 59.95% Indels: 0
DB: Gaps: 0

US-09-659-379-6_COPY_27_175 (1-149) x US-09-997-722-150 (1-528)

QY 1 GIUGLUSERGINLYLSLEUPROSERARGLIETHRCYSPROGLINGYSERVALALA 20
DB 79 GAAGAACCCCAAGGGAATCGCTCTGACGAGATCCGCTGCCAAGGCTCCAAGGCC 138

QY 21 TYRGLYSERTYRCYTYRSEULEULELEPROGINTHRTYRSEASNAJGULEU 40
DB 139 TATGCTCCACTGCTATGCTGTTTGTTCACCAAAATCTGCAGATCCAGATCTG 198

QY 41 SERCYGLIMEHISPHESERGLYHISLEUALAPHELEUSERTHRGYLULETHR 60
DB 199 GCCTGCCAGAGCGCCCTCTGGAACCTGTGCTGCTCAGTGGGCTCAGGGATCC 258

QY 61 PHEVALSERSEULEVALYLSANSERLEUTHRALATYRGLINTYRILETRIPLE 80
DB 259 TTGCTGCTCCTGCTGTAAGACATTTGGTAAACACTACTCATACCTGGAATGGGCTC 318

QY 81 HISAPPROSERHISGLYTHIRLEUPROAENGYSERGLITRIPLETRPSEASNA 100
DB 319 CATGACCCCAAGGCAAGCCCAATGAGAGAGTTGGAGTGGAGTACAGTGTAT 378

QY 101 VALLEUTHPHETYSANTRPGIARGASPROSERILEALALAASPARGLITYR 120
DB 379 GTCATGAATTAATCTTGATGAGAGAAATCCCTCCACATCTCAGGCCGCACTGT 438

QY 121 ALAVALLEUSERGLYSERGYPHEGLINLYSTTPARGASPHASNCYSGIUAENGL 140
DB 439 GCGAGCTGTGCGAAGACACAGCATTTCTGAGGTGGAAGATTATTAATGTGAGG 498

QY 141 LEUPROTYRILECYSLYSPHE 147
DB 499 TTACCTATGTCTGCAAGTTC 519

RESULT 13
US-10-316-761-5
Sequence 5, Application US/10316761
Publication No. US20030109004A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PANCAEATITIS-ASSOCIATED PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/316,761
FILING DATE: 10-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/822,261
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0251 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 797 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 262368
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-316-761-5

Alignment Scores:
Pred. No.: 2,516-56 Length: 797
Score: 491.00 Matches: 82
Percent Similarity: 77.55% Conservative: 32
Best Local Similarity: 55.78% Mismatches: 33
Query Match: 59.95% Indels: 0
DB: Gaps: 0

US-09-659-379-6_COPY_27_175 (1-149) x US-10-316-761-5 (1-797)

QY 1 GIUGLUSERGINLYLSLEUPROSERARGLIETHRCYSPROGLINGYSERVALALA 20
DB 121 GAAGAACCCCAAGGGAATCGCTCTGACGAGATCCGCTGCCAAGGCTCCAAGGCC 180

QY 21 TYRGLYSERTYRCYTYRSEULEULELEPROGINTHRTYRSEASNAJGULEU 40
DB 181 TATGCTCCACTGCTATGCTGTTTGTTCACCAAAATCTGCAGATCCAGATCTG 240

QY 41 SERCYGLIMEHISPHESERGLYHISLEUALAPHELEUSERTHRGYLULETHR 60
DB 241 GCCTGCCAGAGCGCCCTCTGGAACCTGTGCTGCTCAGTGGGCTCAGGGATCC 300

QY 61 PHEVALSERSEULEVALYLSANSERLEUTHRALATYRGLINTYRILETRIPLE 80
DB 301 TTGCTGCTCCTGCTGTAAGACATTTGGTAAACACTACTCATACCTGGAATGGGCTC 360

QY 81 HISAPPROSERHISGLYTHIRLEUPROAENGYSERGLITRIPLETRPSEASNA 100
DB 361 CATGACCCCAAGGCAAGCCCAATGAGAGAGTTGGAGTGGAGTACAGTGTAT 420

QY 101 VALLEUTHPHETYSANTRPGIARGASPROSERILEALALAASPARGLITYR 120
DB 421 GTCATGAATTAATCTTGATGAGAGAAATCCCTCCACATCTCAGGCCGCACTGT 480

QY 121 ALAVALLEUSERGLYSERGYPHEGLINLYSTTPARGASPHASNCYSGIUAENGL 140
DB 481 GCGAGCTGTGCGAAGACACAGCATTTCTGAGGTGGAAGATTATTAATGTGAGG 540

QY 141 LEUPROTYRILECYSLYSPHE 147
DB 541 TTACCTATGTCTGCAAGTTC 561

RESULT 14
US-09-997-722-149

```
; Sequence 149, Application US/09997722
; Publication No. US20040072154A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71171/RMS/DCF
; CURRENT APPLICATION NUMBER: US/09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 149
; LENGTH: 807
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-997-722-149

Alignment Scores:
Pred. No.: 2,55e-56 Length: 807
Score: 491.00 Matches: 82
Percent Similarity: 77.55% Conservative: 32
Best Local Similarity: 55.78% Mismatches: 33
Query Match: 59.95% Indels: 0
Gaps: 0
DB: 12

US-09-659-379-6_COPY_27_175 (1-149) x US-09-997-722-149 (1-807)

QY 1 GluGlnSerGlnuSLySLeuProSerSerArgIleThrCysProGlnGlySerValAla 20
Db 139 GAAAGACCCCAAGAGGAACTGCTCTGACAGATCCGCTCTCCCAAGGCTCCCAAGGCC 198
QY 21 TyrGlySerTyTyTySerSerLeuIleuIleProGlnThrTrpSerAsnAlaGluLeu 40
Db 199 TATGGCTCCCACTGATGCTTGTGTTTGTACCAAAATCTTGACAGATGCAATGCTG 258
QY 41 SerCysGlnMetHisPheSerGlyHisLeuAlaPheLeuLeuSerThrGlyGluIleThr 50
Db 259 GCGTGCCAGAGAGCGCCCTCTGGAACCTGCTGCTGCTCAGTGGGGCTGAGGAGATCC 318
QY 61 PheValSerSerLeuValLysAsnSerLeuThrAlaTyGlnTyIleTrpIleGlyLeu 80
Db 319 TTCGTGCTCTCCCTGGTGAGAGATGTAACAGCTACTCATACGCTTGATTTGGGCTC 378
QY 81 HisAspProSerHisGlyThrLeuProAsnGlySerGlyTyTrpLysTrpSerSerAsn 100
Db 379 CATGACCCCAACAGAGGCAAGGATGAGAGAGGTTGGAGTGGAGTAGCAGTAT 438
QY 101 ValLeuThrPheTyTrpAsnTrpGluArgAsnProSerIleAlaAlaAspArgGlyTyTyCys 120
Db 439 GTGATGATTTACTTTGTCATGGAGAGAAATCCCTCCACATCTCAAGCCCGGCACATGT 498
QY 121 AlaValLeuSerGlnLysSerGlyPheGlnLysTrpPArgAspPheAsnGlyGluAsnGlu 140
Db 499 GCGAGCCCTGTGAGAGAGACAGCATTTCTGAGGTGAGAAAGATTAACTGTAATGTGAG 558
QY 141 LeuProTyIleCysLysPhe 147
Db 559 TTACCTTANGTGCAAGTTTC 579

RESULT 15
US-09-925-301-171
; Sequence 171, Application US/09925301
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
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; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 171
; LENGTH: 940
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (12)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (919)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (935)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (938)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-925-301-171

Alignment Scores:
Pred. No.: 3.2e-56 Length: 940
Score: 491.00 Matches: 82
Percent Similarity: 77.55% Conservative: 32
Best Local Similarity: 55.78% Mismatches: 33
Query Match: 59.95% Indels: 0
Gaps: 0
DB: 9

US-09-659-379-6_COPY_27_175 (1-149) x US-09-925-301-171 (1-940)

QY 1 GluGlnSerGlnuSLySLeuProSerSerArgIleThrCysProGlnGlySerValAla 20
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QY 21 TyrGlySerTyTyTySerSerLeuIleuIleProGlnThrTrpSerAsnAlaGluLeu 40
Db 216 TATGGCTCCCACTGATGCTTGTGTTTGTACCAAAATCTTGACAGATGCAATGCTG 275
QY 41 SerCysGlnMetHisPheSerGlyHisLeuAlaPheLeuLeuSerThrGlyGluIleThr 60
Db 276 GCGTGCCAGAGAGCGCCCTCTGGAACCTGCTGCTGCTCAGTGGGGCTGAGGAGATCC 335
QY 61 PheValSerSerLeuValLysAsnSerLeuThrAlaTyGlnTyIleTrpIleGlyLeu 80
Db 336 TTCGTGCTCTCCCTGGTGAGAGATGTAACAGCTACTCATACGCTTGATTTGGGCTC 395
QY 81 HisAspProSerHisGlyThrLeuProAsnGlySerGlyTyTrpLysTrpSerSerAsn 100
Db 396 CATGACCCCAACAGAGGCAAGGATGAGAGAGGTTGGAGTGGAGTAGCAGTAT 455
QY 101 ValLeuThrPheTyTrpAsnTrpGluArgAsnProSerIleAlaAlaAspArgGlyTyTyCys 120
Db 456 GTGATGATTTACTTTGTCATGGAGAGAAATCCCTCCACATCTCAAGCCCGGCACATGT 515
QY 121 AlaValLeuSerGlnLysSerGlyPheGlnLysTrpPArgAspPheAsnGlyGluAsnGlu 140
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QY 141 LeuProTyIleCysLysPhe 147
Db 576 TTACCTTANGTGCAAGTTTC 596

Search completed: August 8, 2004, 08:13:27
Job time : 418 secs
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